

SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC	48
Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile	
1 5 10 15	
TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC	96
Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly	
20 25 30	
ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG	144
Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
35 40 45	
CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA	192
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg	
50 55 60	
TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC	240
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr	
65 70 75 80	
CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA	288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly	
85 90 95	
GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG	336
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu	
100 105 110	
GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC	384
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr	
115 120 125	
GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC	432
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Ser Leu His Tyr	
130 135 140	
GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG	480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys	
145 150 155 160	

TAC	GGA	ATG	CTG	GCC	CGC	CTC	GCC	GTC	GAG	GCC	GGC	TTC	GAC	TGG	GTC	528
Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
				165					170					175		
TAC	TAC	GAG	TCC	AAG	GCG	CAC	ATC	CAC	TGC	TCC	GTC	AAA	GCA	GAA	AAC	576
Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
				180				185					190			
TCA	GTG	GCA	GCG	AAA	TCA	GGA	GGC	TGC	TTC	CCT	GGC	TCA	GCC	ACA	GTG	624
Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	
				195				200					205			
CAC	CTG	GAG	CAT	GGA	GGC	ACC	AAG	CTG	GTG	AAG	GAC	CTG	AGC	CCT	GGG	672
His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	
				210				215				220				
GAC	CGC	GTG	CTG	GCT	GCT	GAC	GCG	GAC	GGC	CGG	CTG	CTC	TAC	AGT	GAC	720
Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	
						230				235					240	
TTC	CTC	ACC	TTC	CTC	GAC	CGG	ATG	GAC	AGC	TCC	CGA	AAG	CTC	TTC	TAC	768
Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr	
				245				250						255		
GTC	ATC	GAG	ACG	CGG	CAG	CCC	CGG	GCC	CGG	CTG	CTA	CTG	ACG	GCG	GCC	816
Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala	
				260				265					270			
CAC	CTG	CTC	TTT	GTG	GCC	CCC	CAG	CAC	AAC	CAG	TCG	GAG	GCC	ACA	GGG	864
His	Leu	Leu	Phe	Val	Ala	Pro	Gln	His	Asn	Gln	Ser	Glu	Ala	Thr	Gly	
				275				280					285			
TCC	ACC	AGT	GGC	CAG	GCG	CTC	TTC	GCC	AGC	AAC	GTG	AAG	CCT	GGC	CAA	912
Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln	
						295					300					
CGT	GTC	TAT	GTG	CTG	GGC	GAG	GGC	GGG	CAG	CAG	CTG	CTG	CCG	GCG	TCT	960
Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser	
					310					315					320	
GTC	CAC	AGC	GTC	TCA	TTG	CGG	GAG	GAG	GCG	TCC	GGA	GCC	TAC	GCC	CCA	1008
Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro	
					325				330					335		
CTC	ACC	GCC	CAG	GGC	ACC	ATC	CTC	ATC	AAC	CGG	GTG	TTG	GCC	TCC	TGC	1056
Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	
				340				345					350			
TAC	GCC	GTC	ATC	GAG	GAG	CAC	AGT	TGG	GCC	CAT	TGG	GCC	TTC	GCA	CCA	1104
Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro	
				355				360					365			
TTC	CGC	TTG	GCT	CAG	GGG	CTG	CTG	GCC	GCC	CTC	TGC	CCA	GAT	GGG	GCC	1152
Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala	
						375					380					
ATC	CCT	ACT	GCC	GCC	ACC	ACC	ACC	ACT	GGC	ATC	CAT	TGG	TAC	TCA	CGG	1200
Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg	
						390				395					400	
CTC	CTC	TAC	CGC	ATC	GGC	AGC	TGG	GTG	CTG	GAT	GGT	GAC	GCG	CTG	CAT	1248
Leu	Leu	Tyr	Arg	Ile	Gly	Ser	Trp	Val	Leu	Asp	Gly	Asp	Ala	Leu	His	

CGT Arg 145	GCC Ala	TTG Leu	GAC Asp	ATC Ile	ACC Thr 150	ACG Thr	TCT Ser	GAC Asp	CGT Arg	GAC Asp 155	CGT Arg	AAT Asn	AAG Lys	TAT Tyr	GGT Gly 160	480
TTG Leu	TTG Leu	GCG Ala	CGC Arg	CTA Leu 165	GCT Ala	GTG Val	GAA Glu	GCC Ala	GGA Gly 170	TTC Phe	GAC Asp	TGG Trp	GTC Val	TAC Tyr 175	TAC Tyr	528
GAG Glu	TCC Ser	CGC Arg	AAC Asn 180	CAC His	ATC Ile	CAC His	GTA Val	TCG Ser 185	GTC Val	AAA Lys	GCT Ala	GAT Asp	AAC Asn 190	TCA Ser	CTG Leu	576
GCG Ala	GTC Val	CGA Arg 195	GCC Ala	GGA Gly	GGC Gly	TGC Cys	TTT Phe 200	CCG Pro	GGA Gly	AAT Asn	GCC Ala	ACG Thr 205	GTG Val	CGC Arg	TTG Leu	624
CGG Arg	AGC Ser 210	GGC Gly	GAA Glu	CGG Arg	AAG Lys	GGG Gly 215	CTG Leu	AGG Arg	GAA Glu	CTA Leu	CAT His 220	CGT Arg	GGT Gly	GAC Asp	TGG Trp	672
GTA Val 225	CTG Leu	GCC Ala	GCT Ala	GAT Asp 230	GCA Ala	GCG Ala	GGC Gly	CGA Arg	GTG Val	GTA Val 235	CCC Pro	ACG Thr	CCA Pro	GTG Val	CTG Leu 240	720
CTC Leu	TTC Phe	CTG Leu	GAC Asp 245	CGG Arg	GAT Asp	CTG Leu	CAG Gln	CGC Arg 250	CGC Arg	GCC Ala	TCG Ser	TTC Phe	GTG Val 255	GCT Ala 255	GTG Val	768
GAG Glu	ACC Thr	GAG Glu	CGG Arg 260	CCT Pro	CCG Pro	CGC Arg	AAA Lys 265	CTG Leu	TTG Leu	CTC Leu	ACA Thr	CCC Pro 270	TGG Trp 270	CAT His	CTG Leu	816
GTG Val	TTC Phe 275	GCT Ala	GCT Ala	CGC Arg	GGG Gly	CCA Pro 280	GCG Ala	CCT Pro	GCT Ala	CCA Pro	GGT Gly 285	GAC Asp 285	TTT Phe	GCA Ala	CCG Pro	864
GTG Val 290	TTC Phe	GCG Ala	CGC Arg	CGC Arg	TTA Leu	CGT Arg 295	GCT Ala	GGC Gly	GAC Asp	TCG Ser 300	GTG Val	CTG Leu	GCT Ala	CCC Pro	GGC Gly	912
GGG Gly 305	GAC Asp	GCG Ala	CTC Leu	CAG Gln 310	CCG Pro	GCG Ala	CGC Arg	GTA Val	GCC Ala 315	CGC Arg	GTG Val	GCG Ala	CGC Arg	GAG Glu	GAA Glu 320	960
GCC Ala	GTG Val	GGC Gly	GTG Val	TTC Phe 325	GCA Ala	CCG Pro	CTC Leu	ACT Thr	GCG Ala 330	CAC His	GGG Gly	ACG Thr	CTG Leu	CTG Leu 335	GTC Val	1008
AAC Asn	GAC Asp	GTC Val	CTC Leu 340	GCC Ala	TCC Ser	TGC Cys	TAC Tyr 345	GCG Ala	GTT Val	CTA Leu	GAG Glu	AGT Ser 350	CAC His	CAG Gln	TGG Trp	1056
GCC Ala	CAC His 355	CGC Arg	GCC Ala	TTC Phe	GCC Ala	CCT Pro 360	TTG Leu	CGG Arg	CTG Leu	CTG Leu	CAC His 365	GCG Ala 365	CTC Leu	GGG Gly	GCT Ala	1104
CTG Leu	CTC Leu 370	CCT Pro	GGG Gly	GGT Gly	GCA Ala	GTC Val 375	CAG Gln	CCG Pro	ACT Thr	GGC Gly 380	ATG Met	CAT His	TGG Trp	TAC Tyr	TCT Ser	1152

145	150								155								160								
AAT Asn	AAG Lys	TAT Tyr	GGA Gly	CTG Leu	CTG Leu	GCG Ala	CGC Arg	TTA Leu	GCA Ala	GTG Val	GAG Glu	GCC Ala	GGC Gly	TTC Phe	GAC Asp	528									
				165					170					175											
TGG Trp	GTG Val	TAT Tyr	TAC Tyr	GAG Glu	TCC Ser	AAG Lys	GCC Ala	CAC His	GTG Val	CAT His	TGC Cys	TCT Ser	GTC Val	AAG Lys	TCT Ser	576									
				180					185					190											
GAG Glu	CAT His	TCG Ser	GCC Ala	GCT Ala	GCC Ala	AAG Lys	ACA Thr	GGT Gly	GGC Gly	TGC Cys	TTT Phe	CCT Pro	GCC Ala	GGA Gly	GCC Ala	624									
				195					200					205											
CAG Gln	GTG Val	CGC Arg	CTA Leu	GAG Glu	AAC Asn	GGG Gly	GAG Glu	CGT Arg	GTG Val	GCC Ala	CTG Leu	TCA Ser	GCT Ala	GTA Val	AAG Lys	672									
				210					215					220											
CCA Pro	GGA Gly	GAC Asp	CGG Arg	GTG Val	CTG Leu	GCC Ala	ATG Met	GGG Gly	GAG Glu	GAT Asp	GGG Gly	ACC Thr	CCC Pro	ACC Thr	TTC Phe	720									
				225					230					235											
AGT Ser	GAT Asp	GTG Val	CTT Leu	ATT Ile	TTC Phe	CTG Leu	GAC Asp	CGC Arg	GAG Glu	CCA Pro	AAC Asn	CGG Arg	CTG Leu	AGA Arg	GCT Ala	768									
				245					250					255											
TTC Phe	CAG Gln	GTC Val	ATC Ile	GAG Glu	ACT Thr	CAG Gln	GAT Asp	CCT Pro	CCG Pro	CGT Arg	CGG Arg	CTG Leu	GCG Ala	CTC Leu	ACG Thr	816									
				260					265					270											
CCT Pro	GCC Ala	CAC His	CTG Leu	CTC Leu	TTC Phe	ATT Ile	GCG Ala	GAC Asp	AAT Asn	CAT His	ACA Thr	GAA Glu	CCA Pro	GCA Ala	GCC Ala	864									
				275					280					285											
CAC His	TTC Phe	CGG Arg	GCC Ala	ACA Thr	TTT Phe	GCC Ala	AGC Ser	CAT His	GTG Val	CAA Gln	CCA Pro	GGC Gly	CAA Gln	TAT Tyr	GTG Val	912									
				290					295					300											
CTG Leu	GTA Val	TCA Ser	GGG Gly	GTA Val	CCA Pro	GGC Gly	CTC Leu	CAG Gln	CCT Pro	GCT Ala	CGG Arg	GTG Val	GCA Ala	GCT Ala	GTC Val	960									
				305					310					315											
TCC Ser	ACC Thr	CAC His	GTG Val	GCC Ala	CTT Leu	GGG Gly	TCC Ser	TAT Tyr	GCT Ala	CCT Pro	CTC Leu	ACA Thr	AGG Arg	CAT His	GGG Gly	1008									
				325					330					335											
ACA Thr	CTT Leu	GTG Val	GTG Val	GAG Glu	GAT Asp	GTG Val	GTG Val	GCC Ala	TCC Ser	TGC Cys	TTT Phe	GCA Ala	GCT Ala	GTG Val	GCT Ala	1056									
				340					345					350											
GAC Asp	CAC His	CAT His	CTG Leu	GCT Ala	CAG Gln	TTG Leu	GCC Ala	TTC Phe	TGG Trp	CCC Pro	CTG Leu	CGA Arg	CTG Leu	TTT Phe	CCC Pro	1104									
				355					360					365											
AGT Ser	TTG Leu	GCA Ala	TGG Trp	GGC Gly	AGC Ser	TGG Trp	ACC Thr	CCA Pro	AGT Ser	GAG Glu	GGT Gly	GTT Val	CAC His	TCC Ser	TAC Tyr	1152									
				370					375					380											
CCT Pro	CAG Gln	ATG Met	CTC Leu	TAC Tyr	CGC Arg	CTG Leu	GGG Gly	CGT Arg	CTC Leu	TTG Leu	CTA Leu	GAA Glu	GAG Glu	AGC Ser	ACC Thr	1200									
				385					390					395											
				400					405					410											

[illegible]

TTC CAT CCA CTG GGC ATG TCT GGG GCA GGA AGC TGAAGGGACT CTAACCACTG	1253
Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser	
405 410	

CCCTCCTGGA ACTGCTGTGC GTGGATCC	1281
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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG CTG CTG CTG CTG GCC AGA TGT TTT CTG GTG ATC CTT GCT TCC TCG	48
Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser	
1 5 10 15	
CTG CTG GTG TGC CCC GGG CTG GCC TGT GGG CCC GGC AGG GGG TTT GGA	96
Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly	
20 25 30	
AAG AGG CGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT	144
Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe	
35 40 45	
ATT CCC AAC GTA GCC GAG AAG ACC CTA GGG GCC AGC GGC AGA TAT GAA	192
Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu	
50 55 60	
GGG AAG ATC ACA AGA AAC TCC GAA CGA TTT AAG GAA CTC ACC CCC AAT	240
Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn	
65 70 75 80	
TAC AAC CCC GAC ATC ATA TTT AAG GAT GAG GAA AAC ACG GGA GCA GAC	288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp	
85 90 95	
CGG CTG ATG ACT CAG AGG TGC AAA GAC AAG TTA AAT GCC TTG GCC ATC	336
Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile	
100 105 110	
TCT GTG ATG AAC CAG TGG CCT GGA GTG AGG CTG CGA GTG ACC GAG GGC	384
Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
115 120 125	
TGG GAT GAG GAC GGC CAT CAT TCA GAG GAG TCT CTA CAC TAT GAG GGT	432
Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly	
130 135 140	

CCCTCCTGGA ACTGCTGTGC GTGGATCC

CGA Arg 145	GCA Ala	GTG Val	GAC Asp	ATC Ile	ACC Thr 150	ACG Thr	TCC Ser	GAC Asp	CGG Arg	GAC Asp 155	CGC Arg	AGC Ser	AAG Lys	TAC Tyr	GGC Gly 160	480
ATG Met	CTG Leu	GCT Ala	CGC Arg	CTG Leu 165	GCT Ala	GTG Val	GAA Glu	GCA Ala	GGT Gly 170	TTC Phe	GAC Asp	TGG Trp	GTC Val	TAC Tyr 175	TAT Tyr	528
GAA Glu	TCC Ser	AAA Lys	GCT Ala 180	CAC His	ATC Ile	CAC His	TGT Cys	TCT Ser 185	GTG Val	AAA Lys	GCA Ala	GAG Glu	AAC Asn 190	TCC Ser	GTG Val	576
GCG Ala	GCC Ala	AAA Lys 195	TCC Ser	GGC Gly	GGC Gly	TGT Cys	TTC Phe 200	CCG Pro	GGA Gly	TCC Ser	GCC Ala	ACC Thr 205	GTG Val	CAC His	CTG Leu	624
GAG Glu	CAG Gln 210	GGC Gly	GGC Gly	ACC Thr	AAG Lys	CTG Leu 215	GTG Val	AAG Lys	GAC Asp	TTA Leu 220	CGT Arg	CCC Pro	GGA Gly	GAC Asp	CGC Arg	672
GTG Val 225	CTG Leu	GCG Ala	GCT Ala	GAC Asp	GAC Asp 230	CAG Gln	GGC Gly	CGG Arg	CTG Leu 235	CTG Leu	TAC Tyr	AGC Ser	GAC Asp	TTC Phe	CTC Leu 240	720
ACC Thr	TTC Phe	CTG Leu	GAC Asp	CGC Arg 245	GAC Asp	GAA Glu	GGC Gly	GCC Ala	AAG Lys 250	AAG Lys	GTC Val	TTC Phe	TAC Tyr	GTG Val 255	ATC Ile	768
GAG Glu	ACG Thr	CTG Leu	GAG Glu 260	CCG Pro	CGC Arg	GAG Glu	CGC Arg	CTG Leu 265	CTG Leu	CTC Leu	ACC Thr	GCC Ala	GCG Ala 270	CAC His	CTG Leu	816
CTC Leu	TTC Phe	GTG Val 275	GCG Ala	CCG Pro	CAC His	AAC Asn	GAC Asp 280	TCG Ser	GGG Gly	CCC Pro	ACG Thr	CCC Pro 285	GGG Gly	CCA Pro	AGC Ser	864
GCG Ala 290	CTC Leu	TTT Phe	GCC Ala	AGC Ser	CGC Arg	GTG Val 295	CGC Arg	CCC Pro	GGG Gly	CAG Gln 300	CGC Arg	GTG Val	TAC Tyr	GTG Val	GTG Val	912
GCT Ala 305	GAA Glu	CGC Arg	GGC Gly	GGG Gly 310	GAC Asp	CGC Arg	CGG Arg	CTG Leu	CTG Leu	CCC Pro 315	GCC Ala	GCG Ala	GTG Val	CAC His	AGC Ser 320	960
GTG Val	ACG Thr	CTG Leu	CGA Arg	GAG Glu 325	GAG Glu	GAG Glu	GCG Ala	GGC Gly	GCG Ala 330	TAC Tyr	GCG Ala	CCG Pro	CTC Leu	ACG Thr 335	GCG Ala	1008
CAC His	GGC Gly	ACC Thr	ATT Ile 340	CTC Leu	ATC Ile	AAC Asn	CGG Arg	GTG Val 345	CTC Leu	GCC Ala	TCG Ser	TGC Cys 350	TAC Tyr	GCT Ala	GTC Val	1056
ATC Ile	GAG Glu	GAG Glu 355	CAC His	AGC Ser	TGG Trp	GCA Ala	CAC His 360	CGG Arg	GCC Ala	TTC Phe	GCG Ala	CCT Pro 365	TTC Phe	CGC Arg	CTG Leu	1104
GCG Ala	CAC His 370	GCG Ala	CTG Leu	CTG Leu	GCC Ala	GCG Ala 375	CTG Leu	GCA Ala	CCC Pro	GCC Ala 380	CGC Arg	ACG Thr	GAC Asp	GGC Gly	GGG Gly	1152

			100				105				110							
GTA	ATG	AAC	CAC	TGG	CCA	GGG	GTT	AAG	CTG	CGT	GTG	ACA	GAG	GGC	TGG		384	
Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp			
		115				120						125						
GAT	GAG	GAC	GGT	CAC	CAT	TTT	GAA	GAA	TCA	CTC	CAC	TAC	GAG	GGA	AGA		432	
Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg			
		130				135						140						
GCT	GTT	GAT	ATT	ACC	ACC	TCT	GAC	CGA	GAC	AAG	AGC	AAA	TAC	GGG	ACA		480	
Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr			
		145				150						155				160		
CTG	TCT	CGC	CTA	GCT	GTG	GAG	GCT	GGA	TTT	GAC	TGG	GTC	TAT	TAC	GAG		528	
Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu			
				165						170				175				
TCC	AAA	GCC	CAC	ATT	CAT	TGC	TCT	GTC	AAA	GCA	GAA	AAT	TCG	GTT	GCT		576	
Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala			
		180						185						190				
GCG	AAA	TCT	GGG	GGC	TGT	TTC	CCA	GGT	TCG	GCT	CTG	GTC	TCG	CTC	CAG		624	
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln			
		195				200						205						
GAC	GGA	GGA	CAG	AAG	GCC	GTG	AAG	GAC	CTG	AAC	CCC	GGA	GAC	AAG	GTG		672	
Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val			
		210				215						220						
CTG	GCG	GCA	GAC	AGC	GCG	GGA	AAC	CTG	GTG	TTC	AGC	GAC	TTC	ATC	ATG		720	
Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met			
		225				230						235				240		
TTC	ACA	GAC	CGA	GAC	TCC	ACG	ACG	CGA	CGT	GTG	TTT	TAC	GTC	ATA	GAA		768	
Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu			
				245				250						255				
ACG	CAA	GAA	CCC	GTT	GAA	AAG	ATC	ACC	CTC	ACC	GCC	GCT	CAC	CTC	CTT		816	
Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu			
		260						265						270				
TTT	GTC	CTC	GAC	AAC	TCA	ACG	GAA	GAT	CTC	CAC	ACC	ATG	ACC	GCC	GCG		864	
Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala			
		275				280						285						
TAT	GCC	AGC	AGT	GTC	AGA	GCC	GGA	CAA	AAG	GTG	ATG	GTT	GTT	GAT	GAT		912	
Tyr	Ala	Ser	Ser	Val	Arg	Ala	Gly	Gln	Lys	Val	Met	Val	Val	Asp	Asp			
		290				295						300						
AGC	GGT	CAG	CTT	AAA	TCT	GTC	ATC	GTG	CAG	CGG	ATA	TAC	ACG	GAG	GAG		960	
Ser	Gly	Gln	Leu	Lys	Ser	Val	Ile	Val	Gln	Arg	Ile	Tyr	Thr	Glu	Glu			
		305				310				315				320				
CAG</																		

GCG CAT TTG GCC TTC GCG CCC GCC AGG CTC TAT TAT TAC GTG TCA TCA	1104
Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser	
355 360 365	
TTC CTG TCC CCC AAA ACT CCA GCA GTC GGT CCA ATG CGA CTT TAC AAC	1152
Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	
370 375 380	
AGG AGG GGG TCC ACT GGT ACT CCA GGC TCC TGT CAT CAA ATG GGA ACG	1200
Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	
385 390 395 400	
TGG CTT TTG GAC AGC AAC ATG CTT CAT CCT TTG GGG ATG TCA GTA AAC	1248
Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn	
405 410 415	
TCA AGC TG	1256
Ser Ser	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG CTG CTG CTG GCG AGA TGT CTG CTG CTA GTC CTC GTC TCC TCG CTG	48
Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu	
1 5 10 15	
CTG GTA TGC TCG GGA CTG GCG TGC GGA CCG GGC AGG GGG TTC GGG AAG	96
Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	
20 25 30	
AGG AGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT ATC	144
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
35 40 45	
CCC AAT GTG GCC GAG AAG ACC CTA GGC GCC AGC GGA AGG TAT GAA GGG	192
Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
50 55 60	
AAG ATC TCC AGA AAC TCC GAG CGA TTT AAG GAA CTC ACC CCC AAT TAC	240
Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	
65 70 75 80	
AAC CCC GAC ATC ATA TTT AAG GAT GAA GAA AAC ACC GGA GCG GAC AGG	288

Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg	
CTG Leu	ATG Met	ACT Thr	CAG Gln 100	AGG Arg	TGT Cys	AAG Lys	GAC Asp	AAG Lys 105	TTG Leu	AAC Asn	GCT Ala	TTG Leu	GCC Ala 110	ATC Ile	TCG Ser	336
GTG Val	ATG Met	AAC Asn 115	CAG Gln	TGG Trp	CCA Pro	GGA Gly	GTG Val 120	AAA Lys	CTG Leu	CGG Arg	GTG Val	ACC Thr 125	GAG Glu	GGC Gly	TGG Trp	384
GAC Asp	GAA Glu 130	GAT Asp	GGC Gly	CAC His	CAC His	TCA Ser 135	GAG Glu	GAG Glu	TCT Ser	CTG Leu	CAC His 140	TAC Tyr	GAG Glu	GGC Gly	CGC Arg	432
GCA Ala 145	GTG Val	GAC Asp	ATC Ile	ACC Thr	ACG Thr 150	TCT Ser	GAC Asp	CGC Arg	GAC Asp	CGC Arg 155	AGC Ser	AAG Lys	TAC Tyr	GGC Gly	ATG Met 160	480
CTG Leu	GCC Ala	CGC Arg	CTG Leu	GCG Ala 165	GTG Val	GAG Glu	GCC Ala	GGC Gly	TTC Phe 170	GAC Asp	TGG Trp	GTG Val	TAC Tyr 175	TAC Tyr	GAG Glu	528
TCC Ser	AAG Lys	GCA Ala	CAT His 180	ATC Ile	CAC His	TGC Cys	TCG Ser	GTG Val 185	AAA Lys	GCA Ala	GAG Glu	AAC Asn	TCG Ser 190	GTG Val	GCG Ala	576
GCC Ala	AAA Lys 195	TCG Ser	GGA Gly	GGC Gly	TGC Cys	TTC Phe	CCG Pro 200	GGC Gly	TCG Ser	GCC Ala	ACG Thr	GTG Val 205	CAC His	CTG Leu	GAG Glu	624
CAG Gln	GGC Gly 210	GGC Gly	ACC Thr	AAG Lys	CTG Leu	GTG Val 215	AAG Lys	GAC Asp	CTG Leu	AGC Ser	CCC Pro 220	GGG Gly	GAC Asp	CGC Arg	GTG Val	672
CTG Leu 225	GCG Ala	GCG Ala	GAC Asp	GAC Asp	CAG Gln 230	GGC Gly	CGG Arg	CTG Leu	CTC Leu	TAC Tyr 235	AGC Ser	GAC Asp	TTC Phe	CTC Leu 240	ACT Thr	720
TTC Phe	CTG Leu	GAC Asp	CGC Arg	GAC Asp 245	GAC Asp	GGC Gly	GCC Ala	AAG Lys	AAG Lys 250	GTC Val	TTC Phe	TAC Tyr	GTG Val 255	ATC Ile	GAG Glu	768
ACG Thr	CGG Arg	GAG Glu	CCG Pro 260	CGC Arg	GAG Glu	CGC Arg	CTG Leu	CTG Leu 265	CTC Leu	ACC Thr	GCC Ala	GCG Ala 270	CAC His	CTG Leu	CTC Leu	816
TTT Phe	GTG Val	GCG Ala 275	CCG Pro	CAC His	AAC Asn	GAC Asp	TCG Ser	GCC Gly	ACC Ala	GGG Gly	GAG Glu	CCC Pro 285	GAG Glu	GCG Ala	TCC Ser	864
TCG Ser	GGC Gly 290	TCG Ser	GGG Gly	CCG Pro	CCT Pro	TCC Ser 295	GGG Gly	GGC Gly	GCA Ala	CTG Leu	GGG Gly 300	CCT Pro	CGG Arg	GCG Ala	CTG Leu	912
TTC Phe 305	GCC Ala	AGC Ser	CGC Arg	GTG Val	CGC Arg 310	CCG Pro	GGC Gly	CAG Gln	CGC Arg	GTG Val 315	TAC Tyr	GTG Val	GTG Val	GCC Ala	GAG Glu 320	960
CGT Arg	GAC Asp	GGG Gly	GAC Asp	CGC Arg	CGG Arg	CTC Leu	CTG Leu	CCC Pro	GCC Ala	GCT Ala	GTG Val	CAC His	AGC Ser	GTG Val	ACC Thr	1008

325										330					335					
CTA	AGC	GAG	GAG	GCC	GCG	GGC	GCC	TAC	GCG	CCG	CTC	ACG	GCC	CAG	GGC	1056				
Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly					
340				345				350												
ACC	ATT	CTC	ATC	AAC	CGG	GTG	CTG	GCC	TCG	TGC	TAC	GCG	GTC	ATC	GAG	1104				
Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu					
355				360				365												
GAG	CAC	AGC	TGG	GCG	CAC	CGG	GCC	TTC	GCG	CCC	TTC	CGC	CTG	GCG	CAC	1152				
Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His					
370				375				380												
GCG	CTC	CTG	GCT	GCA	CTG	GCG	CCC	GCG	CGC	ACG	GAC	CGC	GGC	GGG	GAC	1200				
Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Arg	Gly	Gly	Asp					
385				390				395				400								
AGC	GGC	GGC	GGG	GAC	CGC	GGG	GGC	GGC	GGC	AGA	GTA	GCC	CTA	ACC	1248					
Ser	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr						
405				410				415												
GCT	CCA	GGT	GCT	GCC	GAC	GCT	CCG	GGT	GCG	GGG	GCC	ACC	GCG	GGC	ATC	1296				
Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile					
420				425				430												
CAC	TGG	TAC	TCG	CAG	CTG	CTC	TAC	CAA	ATA	GGC	ACC	TGG	CTC	CTG	GAC	1344				
His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp					
435				440				445												
AGC	GAG	GCC	CTG	CAC	CCG	CTG	GGC	ATG	GCG	GTC	AAG	TCC	AGC	NNN	AGC	1392				
Ser	Glu	Ala	Leu	His	Pro	Leu	Gly	Met	Ala	Val	Lys	Ser	Ser	Xaa	Ser					
450				455				460												
CGG	GGG	GCC	GGG	GGA	GGG	GCG	CGG	GAG	GGG	GCC						1425				
Arg	Gly	Ala	Gly	Gly	Gly	Ala	Arg	Glu	Gly	Ala										
465				470				475												

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 51..1283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CATCAGCCCA	CCAGGAGACC	TCGCCCGCCG	CTCCCCCGGG	CTCCCCGGCC	ATG	TCT	56
					Met	Ser	
					1		

CCC	GCC	CGG	CTC	CGG	CCC	CGA	CTG	CAC	TTC	TGC	CTG	GTC	CTG	TTG	CTG	104
Pro	Ala	Arg	Leu	Arg	Pro	Arg	Leu	His	Phe	Cys	Leu	Val	Leu	Leu	Leu	
		5					10					15				
CTG	CTG	GTG	GTG	CCC	GCG	GCA	TGG	GGC	TGC	GGG	CCG	GGT	CGG	GTG	GTG	152
Leu	Leu	Val	Val	Pro	Ala	Ala	Trp	Gly	Cys	Gly	Pro	Gly	Arg	Val	Val	
	20					25					30					
GGC	AGC	CGC	CGG	CGA	CCG	CCA	CGC	AAA	CTC	GTG	CCG	CTC	GCC	TAC	AAG	200
Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	Tyr	Lys	
	35				40				45						50	
CAG	TTC	AGC	CCC	AAT	GTG	CCC	GAG	AAG	ACC	CTG	GGC	GCC	AGC	GGA	CGC	248
Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
				55					60					65		
TAT	GAA	GGC	AAG	ATC	GCT	CGC	AGC	TCC	GAG	CGC	TTC	AAG	GAG	CTC	ACC	296
Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	
			70					75					80			
CCC	AAT	TAC	AAT	CCA	GAC	ATC	ATC	TTC	AAG	GAC	GAG	GAG	AAC	ACA	GGC	344
Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
		85					90					95				
GCC	GAC	CGC	CTC	ATG	ACC	CAG	CGC	TGC	AAG	GAC	CGC	CTG	AAC	TCG	CTG	392
Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	Ser	Leu	
	100					105					110					
GCT	ATC	TCG	GTG	ATG	AAC	CAG	TGG	CCC	GGT	GTG	AAG	CTG	CGG	GTG	ACC	440
Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
	115				120				125						130	
GAG	GGC	TGG	GAC	GAG	GAC	GGC	CAC	CAC	TCA	GAG	GAG	TCC	CTG	CAT	TAT	488
Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	
				135					140					145		
GAG	GGC	CGC	GCG	GTG	GAC	ATC	ACC	ACA	TCA	GAC	CGC	GAC	CGC	AAT	AAG	536
Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	
			150					155					160			
TAT	GGA	CTG	CTG	GCG	CGC	TTG	GCA	GTG	GAG	GCC	GGC	TTT	GAC	TGG	GTG	584
Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
		165				170						175				
TAT	TAC	GAG	TCA	AAG	GCC	CAC	GTG	CAT	TGC	TCC	GTC	AAG	TCC	GAG	CAC	632
Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	Glu	His	
	180					185					190					
TCG	GCC	GCA	GCC	AAG	ACG	GGC	GGC	TGC	TTC	CCT	GCC	GGA	GCC	CAG	GTA	680
Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	Gln	Val	
	195				200					205					210	
CGC	CTG	GAG	AGT	GGG	GCG	CGT	GTG	GCC	TTG	TCA	GCC	GTG	AGG	CCG	GGA	728
Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly	
				215					220					225		
GAC	CGT	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	AGC	CCC	ACC	TTC	AGC	GAT	776
Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	Ser	Asp	
			230					235					240			

GTG	CTC	ATT	TTC	CTG	GAC	CGC	GAG	CCC	CAC	AGG	CTG	AGA	GCC	TTC	CAG	824	
Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala	Phe	Gln		
		245					250					255					
GTC	ATC	GAG	ACT	CAG	GAC	CCC	CCA	CGC	CGC	CTG	GCA	CTC	ACA	CCC	GCT	872	
Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala		
		260				265					270						
CAC	CTG	CTC	TTT	ACG	GCT	GAC	AAT	CAC	ACG	GAG	CCG	GCA	GCC	CGC	TTC	920	
His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	Arg	Phe		
					280					285					290		
CGG	GCC	ACA	TTT	GCC	AGC	CAC	GTG	CAG	CCT	GGC	CAG	TAC	GTG	CTG	GTG	968	
Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	Leu	Val		
				295					300					305			
GCT	GGG	GTG	CCA	GGC	CTG	CAG	CCT	GCC	CGC	GTG	GCA	GCT	GTC	TCT	ACA	1016	
Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	Ser	Thr		
			310					315					320				
CAC	GTG	GCC	CTC	GGG	GCC	TAC	GCC	CCG	CTC	ACA	AAG	CAT	GGG	ACA	CTG	1064	
His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly	Thr	Leu		
		325					330					335					
GTG	GTG	GAG	GAT	GTG	GTG	GCA	TCC	TGC	TTC	GCG	GCC	GTG	GCT	GAC	CAC	1112	
Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	Asp	His		
		340				345					350						
CAC	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	AGA	CTC	TTT	CAC	AGC	TTG	1160	
His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	Ser	Leu		
		355			360					365					370		
GCA	TGG	GGC	AGC	TGG	ACC	CCG	GGG	GAG	GGT	GTG	CAT	TGG	TAC	CCC	CAG	1208	
Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr	Pro	Gln		
				375					380					385			
CTG	CTC	TAC	CGC	CTG	GGG	CGT	CTC	CTG	CTA	GAA	GAG	GGC	AGC	TTC	CAC	1256	
Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser	Phe	His		
			390					395					400				
CCA	CTG	GGC	ATG	TCC	GGG	GCA	GGG	AGC	TGAAAGGACT			CCACCGCTGC				1303	
Pro	Leu	Gly	Met	Ser	Gly	Ala	Gly	Ser									
		405					410										
CCTCCTGGAA			CTGCTGTACT			GGGTCCAGAA			GCCTCTCAGC			CAGGAGGGAG			CTGGCCCTGG		1363
AAGGGACCTG			AGCTGGGGGA			CACTGGCTCC			TGCCATCTCC			TCTGCCATGA			AGATACACCA		1423
TTGAGACTTG			ACTGGGCAAC			ACCAGCGTCC			CCCACCCGCG			TCGTGGTGTA			GTCATAGAGC		1483

(2) INFORMATION FOR SEQ ID NO:8:

(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG	48
Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
1 5 10 15	
GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG	96
Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	
20 25 30	
CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT	144
Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	
35 40 45	
GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG	192
Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	
50 55 60	
GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC	240
Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
65 70 75 80	
TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC	288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
85 90 95	
CGC CTG ATG ACC GAG CGT TGC AAG GAG AGG GTG AAC GCT TTG GCC ATT	336
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	
100 105 110	
GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC	384
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
115 120 125	
TGG GAC GAG GAC GGC CAC CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC	432
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
130 135 140	
CGT GCT TTG GAC ATC ACT ACG TCT GAC CGC GAC CGC AAC AAG TAT GGG	480
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
145 150 155 160	
TTG CTG GCG CGC CTC GCA GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC	528
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
165 170 175	
GAG TCC CGC AAC CAC GTC CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG	576
Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
180 185 190	

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GCG GTC CGG GCG GGC GGC TGC TTT CCG GGA AAT GCA ACT GTG CGC CTG Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu 195 200 205	624
TGG AGC GGC GAG CGG AAA GGG CTG CGG GAA CTG CAC CGC GGA GAC TGG Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp 210 215 220	672
GTT TTG GCG GCC GAT GCG TCA GGC CGG GTG GTG CCC ACG CCG GTG CTG Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu 225 230 235 240	720
CTC TTC CTG GAC CGG GAC TTG CAG CGC CGG GCT TCA TTT GTG GCT GTG Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val 245 250 255	768
GAG ACC GAG TGG CCT CCA CGC AAA CTG TTG CTC ACG CCC TGG CAC CTG Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu 260 265 270	816
GTG TTT GCC GCT CGA GGG CCG GCG CCC GCG CCA GGC GAC TTT GCA CCG Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro 275 280 285	864
GTG TTC GCG CGC CGG CTA CGC GCT GGG GAC TCG GTG CTG GCG CCC GGC Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly 290 295 300	912
GGG GAT GCG CTT CGG CCA GCG CGC GTG GCC CGT GTG GCG CGG GAG GAA Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu 305 310 315 320	960
GCC GTG GGC GTG TTC GCG CCG CTC ACC GCG CAC GGG ACG CTG CTG GTG Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val 325 330 335	1008
AAC GAT GTC CTG GCC TCT TGC TAC GCG GTT CTG GAG AGT CAC CAG TGG Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp 340 345 350	1056
GCG CAC CGC GCT TTT GCC CCC TTG AGA CTG CTG CAC GCG CTA GGG GCG Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala 355 360 365	1104
CTG CTC CCC GGC GGG GCC GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser 370 375 380	1152
CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GGC TG Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly 385 390 395	1191

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC	48
Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile	
1 5 10 15	
AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT	96
Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly	
20 25 30	
TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG	144
Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
35 40 45	
CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA	192
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys	
50 55 60	
TAC GAA GGC AAA ATC ACA AGG AAT TCA GAG AGA TTT AAA GAG CTG ATT	240
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile	
65 70 75 80	
CCG AAT TAT AAT CCC GAT ATC ATC TTT AAG GAC GAG GAA AAC ACA AAC	288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn	
85 90 95	
GCT GAC AGG CTG ATG ACC AAG CGC TGT AAG GAC AAG TTA AAT TCG TTG	336
Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu	
100 105 110	
GCC ATA TCC GTC ATG AAC CAC TGG CCC GGC GTG AAA CTG CGC GTC ACT	384
Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr	
115 120 125	
GAA GGC TGG GAT GAG GAT GGT CAC CAT TTA GAA GAA TCT TTG CAC TAT	432
Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr	
130 135 140	
GAG GGA CGG GCA GTG GAC ATC ACT ACC TCA GAC AGG GAT AAA AGC AAG	480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys	
145 150 155 160	
TAT GGG ATG CTA TCC AGG CTT GCA GTG GAG GCA GGA TTC GAC TGG GTC	528
Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
165 170 175	
TAT TAT GAA TCT AAA GCC CAC ATA CAC TGC TCT GTC AAA GCA GAA AAT	576
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
180 185 190	
TCA GTG GCT GCT AAA TCA GGA GGA TGT TTT CCT GGG TCT GGG ACG GTG	624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val	

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195	200	205	
ACA CTT GGT GAT GGG ACG AGG AAA CCC ATC AAA GAT CTT AAA GTG GGC			672
Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly			
210	215	220	
GAC CGG GTT TTG GCT GCA GAC GAG AAG GGA AAT GTC TTA ATA AGC GAC			720
Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp			
225	230	235	240
TTT ATT ATG TTT ATA GAC CAC GAT CCG ACA ACG AGA AGG CAA TTC ATC			768
Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile			
245	250	255	
GTC ATC GAG ACG TCA GAA CCT TTC ACC AAG CTC ACC CTC ACT GCC GCG			816
Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala			
260	265	270	
CAC CTA GTT TTC GTT GGA AAC TCT TCA GCA GCT TCG GGT ATA ACA GCA			864
His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala			
275	280	285	
ACA TTT GCC AGC AAC GTG AAG CCT GGA GAT ACA GTT TTA GTG TGG GAA			912
Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu			
290	295	300	
GAC ACA TGC GAG AGC CTC AAG AGC GTT ACA GTG AAA AGG ATT TAC ACT			960
Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr			
305	310	315	320
GAG GAG CAC GAG GGC TCT TTT GCG CCA GTC ACC GCG CAC GGA ACC ATA			1008
Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile			
325	330	335	
ATA GTG GAT CAG GTG TTG GCA TCG TGC TAC GCG GTC ATT GAG AAC CAC			1056
Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His			
340	345	350	
AAA TGG GCA CAT TGG GCT TTT GCG CCG GTC AGG TTG TGT CAC AAG CTG			1104
Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu			
355	360	365	
ATG ACG TGG CTT TTT CCG GCT CGT GAA TCA AAC GTC AAT TTT CAG GAG			1152
Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu			
370	375	380	
GAT GGT ATC CAC TGG TAC TCA AAT ATG CTG TTT CAC ATC GGC TCT TGG			1200
Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp			
385	390	395	400
CTG CTG GAC AGA GAC TCT TTC CAT CCA CTC GGG ATT TTA CAC TTA AGT			1248
Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser			
405	410	415	
TGA			1251

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln
290						295					300				
Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser
305					310					315					320
Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro
				325					330					335	
Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys
			340					345					350		
Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro
		355					360					365			
Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala
370						375					380				
Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg
385					390					395					400
Leu	Leu	Tyr	Arg	Ile	Gly	Ser	Trp	Val	Leu	Asp	Gly	Asp	Ala	Leu	His
				405					410					415	
Pro	Leu	Gly	Met	Val	Ala	Pro	Ala	Ser							
			420					425							

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Leu	Pro	Ala	Ser	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
1				5					10					15	
Ala	Leu	Ser	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
			20					25					30		
Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
		35					40					45			
Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
	50					55					60				
Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
65					70					75					80
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
				85					90					95	
Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile

100					105					110					
Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
115					120					125					
Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
130					135					140					
Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
145					150					155					
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
165					170					175					
Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
180					185					190					
Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
195					200					205					
Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
210					215					220					
Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
225					230					235					
Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
245					250					255					
Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
260					265					270					
Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
275					280					285					
Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
290					295					300					
Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu
305					310					315					
Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val
325					330					335					
Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp
340					345					350					
Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala
355					360					365					
Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser
370					375					380					
Arg	Leu	Leu	Tyr	Arg	Leu	Ala	Glu	Glu	Leu	Met	Gly				
385					390					395					

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
 1           5           10           15
Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
 20           25           30
Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35           40           45
Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50           55           60
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65           70           75           80
Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85           90           95
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100           105           110
Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115           120           125
Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130           135           140
His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145           150           155           160
Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
165           170           175
Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
180           185           190
Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
195           200           205
Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
210           215           220
Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
225           230           235           240
Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
245           250           255
Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
260           265           270
Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
```

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Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
		115					120						125			
Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	
	130					135					140					
Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	
145					150					155					160	
Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
			165						170					175		
Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	
		180						185					190			
Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	
		195					200						205			
Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg	
	210					215					220					
Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	
225					230					235					240	
Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	
			245						250					255		
Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	
		260						265					270			
Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser	
	275					280						285				
Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	
	290					295					300					
Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	
305					310					315					320	
Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	
			325					330						335		
His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	
		340						345					350			
Ile	Glu	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	
		355					360					365				
Ala	His	Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Gly	Gly	
	370					375					380					
Gly	Gly	Gly	Ser	Ile	Pro	Ala	Ala	Gln	Ser	Ala	Thr	Glu	Ala	Arg	Gly	
385					390					395					400	
Ala	Glu	Pro	Thr	Ala	Gly	Ile	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	His	
			405						410					415		
Ile	Gly	Thr	Trp	Leu	Leu	Asp	Ser	Glu	Thr	Met	His	Pro	Leu	Gly	Met	
		420						425					430			

[illegible]

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Leu	Leu	Leu	Ala	Arg	Cys	Leu	Leu	Leu	Val	Leu	Val	Ser	Ser	Leu
1				5					10					15	
Leu	Val	Cys	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	Lys
			20					25					30		
Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile
		35					40					45			
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly

Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
385 390 395 400

Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
405 410 415

Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
420 425 430

His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
435 440 445

Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
450 455 460

Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
465 470 475

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
1 5 10 15

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125

Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp

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165								170				175			
Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser
			180					185					190		
Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala
		195					200					205			
Gln	Val	Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg
	210					215					220				
Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe
225					230					235					240
Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala
				245					250					255	
Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr
			260					265					270		
Pro	Ala	His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala
		275					280					285			
Arg	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val
	290					295					300				
Leu	Val	Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val
305					310					315					320
Ser	Thr	His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly
				325					330					335	
Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala
			340					345					350		
Asp	His	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His
		355					360					365			
Ser	Leu	Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr
	370					375					380				
Pro	Gln	Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser
385					390					395					400
Phe	His	Pro	Leu	Gly	Met	Ser	Gly	Ala	Gly	Ser					
				405					410						

(2) INFORMATION FOR SEQ ID NO:17:

(ii) MOLECULE TYPE: protein

Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15

Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg		
			20					25					30				
Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe		
		35					40					45					
Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu		
	50					55					60						
Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn		
	65				70				75						80		
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp		
				85					90					95			
Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile		
			100					105					110				
Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly		
		115					120					125					
Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly		
	130					135					140						
Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly		
	145				150					155					160		
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr		
				165					170					175			
Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu		
			180					185					190				
Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu		
		195					200					205					
Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp		
	210					215					220						
Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu		
	225				230					235					240		
Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val		
			245						250					255			
Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu		
			260					265					270				
Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro		
		275					280					285					
Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly		
	290					295					300						
Gly	Asp	Ala	Leu	Arg	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu		
	305				310					315				320			
Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val		
				325					330					335			
Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp		

340

345

350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
 385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
 20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
 50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
 65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
 85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
 100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
 130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
 145 150 155 160

Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val

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195	200	205
Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly		
210	215	220
Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp		
225	230	235 240
Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile		
	245	250 255
Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala		
	260	265 270
His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala		
	275	280 285
Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu		
	290	295 300
Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr		
305	310	315 320
Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile		
	325	330 335
Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His		
	340	345 350
Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu		
	355	360 365
Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu		
	370	375 380
Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp		
385	390	395 400
Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser		
	405	410 415

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GAT AAC CAC AGC TCA GTG CCT TGG GCC AGT GCC GCC AGT GTC ACC

Met	Asp	Asn	His	Ser	Ser	Val	Pro	Trp	Ala	Ser	Ala	Ala	Ser	Val	Thr	
1				5					10					15		
TGT	CTC	TCC	CTG	GGA	TGC	CAA	ATG	CCA	CAG	TTC	CAG	TTC	CAG	TTC	CAG	96
Cys	Leu	Ser	Leu	Gly	Cys	Gln	Met	Pro	Gln	Phe	Gln	Phe	Gln	Phe	Gln	
			20					25					30			
CTC	CAA	ATC	CGC	AGC	GAG	CTC	CAT	CTC	CGC	AAG	CCC	GCA	AGA	AGA	ACG	144
Leu	Gln	Ile	Arg	Ser	Glu	Leu	His	Leu	Arg	Lys	Pro	Ala	Arg	Arg	Thr	
		35					40					45				
CAA	ACG	ATG	CGC	CAC	ATT	GCG	CAT	ACG	CAG	CGT	TGC	CTC	AGC	AGG	CTG	192
Gln	Thr	Met	Arg	His	Ile	Ala	His	Thr	Gln	Arg	Cys	Leu	Ser	Arg	Leu	
	50					55					60					
ACC	TCT	CTG	GTG	GCC	CTG	CTG	CTG	ATC	GTC	TTG	CCG	ATG	GTC	TTT	AGC	240
Thr	Ser	Leu	Val	Ala	Leu	Leu	Leu	Ile	Val	Leu	Pro	Met	Val	Phe	Ser	
	65				70				75						80	
CCG	GCT	CAC	AGC	TGC	GGT	CCT	GGC	CGA	GGA	TTG	GGT	CGT	CAT	AGG	GCG	288
Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala	
				85					90					95		
CGC	AAC	CTG	TAT	CCG	CTG	GTC	CTC	AAG	CAG	ACA	ATT	CCC	AAT	CTA	TCC	336
Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser	
			100					105					110			
GAG	TAC	ACG	AAC	AGC	GCC	TCC	GGA	CCT	CTG	GAG	GGT	GTG	ATC	CGT	CGG	384
Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg	
		115					120					125				
GAT	TCG	CCC	AAA	TTC	AAG	GAC	CTC	GTG	CCC	AAC	TAC	AAC	AGG	GAC	ATC	432
Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile	
	130					135					140					
CTT	TTC	CGT	GAC	GAG	GAA	GGC	ACC	GGA	GCG	GAT	GGC	TTG	ATG	AGC	AAG	480
Leu	Phe	Arg	Asp	Glu	Glu	Gly	Thr	Gly	Ala	Asp	Gly	Leu	Met	Ser	Lys	
	145				150					155					160	
CGC	TGC	AAG	GAG	AAG	CTA	AAC	GTG	CTG	GCC	TAC	TCG	GTG	ATG	AAC	GAA	528
Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu	
				165					170						175	
TGG	CCC	GGC	ATC	CGG	CTG	CTG	GTC	ACC	GAG	AGC	TGG	GAC	GAG	GAC	TAC	576
Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr	
			180					185					190			
CAT	CAC	GGC	CAG	GAG	TCG	CTC	CAC	TAC	GAG	GGC	CGA	GCG	GTG	ACC	ATT	624
His	His	Gly	Gln	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Thr	Ile	
		195					200					205				
GCC	ACC	TCC	GAT	CGC	GAC	CAG	TCC	AAA	TAC	GGC	ATG	CTC	GCT	CGC	CTG	672
Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu	
	210					215					220					
GCC	GTC	GAG	GCT	GGA	TTC	GAT	TGG	GTC	TCC	TAC	GTC	AGC	AGG	CGC	CAC	720
Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His	
	225				230					235					240	
ATC	TAC	TGC	TCC	GTC	AAG	TCA	GAT	TCG	TCG	ATC	AGT	TCC	CAC	GTG	CAC	768
Ile	Tyr	Cys	Ser	Val	Lys	Ser	Asp	Ser	Ser	Ile	Ser	Ser	His	Val	His	

				245					250					255				
GGC	TGC	TTC	ACG	CCG	GAG	AGC	ACA	GCG	CTG	CTG	GAG	AGT	GGA	GTC	CGG			816
Gly	Cys	Phe	Thr	Pro	Glu	Ser	Thr	Ala	Leu	Leu	Glu	Ser	Gly	Val	Arg			
			260					265					270					
AAG	CCG	CTC	GGC	GAG	CTC	TCT	ATC	GGA	GAT	CGT	GTT	TTG	AGC	ATG	ACC			864
Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr			
		275					280					285						
GCC	AAC	GGA	CAG	GCC	GTC	TAC	AGC	GAA	GTG	ATC	CTC	TTC	ATG	GAC	CGC			912
Ala	Asn	Gly	Gln	Ala	Val	Tyr	Ser	Glu	Val	Ile	Leu	Phe	Met	Asp	Arg			
	290					295					300							
AAC	CTC	GAG	CAG	ATG	CAA	AAC	TTT	GTG	CAG	CTG	CAC	ACG	GAC	GGT	GGA			960
Asn	Leu	Glu	Gln	Met	Gln	Asn	Phe	Val	Gln	Leu	His	Thr	Asp	Gly	Gly			
305					310				315					320				
GCA	GTG	CTC	ACG	GTG	ACG	CCG	GCT	CAC	CTG	GTT	AGC	GTT	TGG	CAG	CCG			1008
Ala	Val	Leu	Thr	Val	Thr	Pro	Ala	His	Leu	Val	Ser	Val	Trp	Gln	Pro			
			325					330					335					
GAG	AGC	CAG	AAG	CTC	ACG	TTT	GTG	TTT	GCG	CAT	CGC	ATC	GAG	GAG	AAG			1056
Glu	Ser	Gln	Lys	Leu	Thr	Phe	Val	Phe	Ala	His	Arg	Ile	Glu	Glu	Lys			
			340					345					350					
AAC	CAG	GTG	CTC	GTA	CGG	GAT	GTG	GAG	ACG	GGC	GAG	CTG	AGG	CCC	CAG			1104
Asn	Gln	Val	Leu	Val	Arg	Asp	Val	Glu	Thr	Gly	Glu	Leu	Arg	Pro	Gln			
		355				360						365						
CGA	GTG	GTC	AAG	TTG	GGC	AGT	GTG	CGC	AGT	AAG	GGC	GTG	GTC	GCG	CCG			1152
Arg	Val	Val	Lys	Leu	Gly	Ser	Val	Arg	Ser	Lys	Gly	Val	Val	Ala	Pro			
	370					375					380							
CTG	ACC	CGC	GAG	GGC	ACC	ATT	GTG	GTC	AAC	TCG	GTG	GCC	GCC	AGT	TGC			1200
Leu	Thr	Arg	Glu	Gly	Thr	Ile	Val	Val	Asn	Ser	Val	Ala	Ala	Ser	Cys			
385					390				395						400			
TAT	GCG	GTG	ATC	AAC	AGT	CAG	TCG	CTG	GCC	CAC	TGG	GGA	CTG	GCT	CCC			1248
Tyr	Ala	Val	Ile	Asn	Ser	Gln	Ser	Leu	Ala	His	Trp	Gly	Leu	Ala	Pro			
				405				410					415					
ATG	CGC	CTG	CTG	TCC	ACG	CTG	GAG	GCG	TGG	CTG	CCC	GCC	AAG	GAG	CAG			1296
Met	Arg	Leu	Leu	Ser	Thr	Leu	Glu	Ala	Trp	Leu	Pro	Ala	Lys	Glu	Gln			
			420				425						430					
TTG	CAC	AGT	TCG	CCG	AAG	GTG	GTG	AGC	TCG	GCG	CAG	CAG	CAG	AAT	GGC			1344
Leu	His	Ser	Ser	Pro	Lys	Val	Val	Ser	Ser	Ala	Gln	Gln	Gln	Asn	Gly			
		435				440						445						
ATC	CAT	TGG	TAT	GCC	AAT	GCG	CTC	TAC	AAG	GTC	AAG	GAC	TAC	GTG	CTG			1392
Ile	His	Trp	Tyr	Ala	Asn	Ala	Leu	Tyr	Lys	Val	Lys	Asp	Tyr	Val	Leu			
	450				455						460							
CCG	CAG	AGC	TGG	CGC	CAC	GAT	TGA											1416
Pro	Gln	Ser	Trp	Arg	His	Asp												
465					470													

(2) INFORMATION FOR SEQ ID NO:20:

[illegible]

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

Met 1	Asp	Asn	His	Ser 5	Ser	Val	Pro	Trp	Ala 10	Ser	Ala	Ala	Ser	Val	Thr
Cys	Leu	Ser	Leu 20	Gly	Cys	Gln	Met	Pro 25	Gln	Phe	Gln	Phe	Gln 30	Phe	Gln
Leu	Gln	Ile 35	Arg	Ser	Glu	Leu	His 40	Leu	Arg	Lys	Pro	Ala 45	Arg	Arg	Thr
Gln	Thr 50	Met	Arg	His	Ile	Ala 55	His	Thr	Gln	Arg	Cys 60	Leu	Ser	Arg	Leu
Thr 65	Ser	Leu	Val	Ala	Leu 70	Leu	Leu	Ile	Val	Leu 75	Pro	Met	Val	Phe	Ser 80
Pro	Ala	His	Ser	Cys 85	Gly	Pro	Gly	Arg	Gly 90	Leu	Gly	Arg	His	Arg 95	Ala
Arg	Asn	Leu	Tyr 100	Pro	Leu	Val	Leu	Lys 105	Gln	Thr	Ile	Pro	Asn 110	Leu	Ser
Glu	Tyr	Thr 115	Asn	Ser	Ala	Ser	Gly 120	Pro	Leu	Glu	Gly	Val 125	Ile	Arg	Arg
Asp 130	Ser	Pro	Lys	Phe	Lys	Asp 135	Leu	Val	Pro	Asn	Tyr 140	Asn	Arg	Asp	Ile
Leu 145	Phe	Arg	Asp	Glu	Glu 150	Gly	Thr	Gly	Ala	Asp 155	Gly	Leu	Met	Ser	Lys 160
Arg	Cys	Lys	Glu	Lys 165	Leu	Asn	Val	Leu	Ala 170	Tyr	Ser	Val	Met	Asn 175	Glu
Trp	Pro	Gly 180	Ile	Arg	Leu	Leu	Val	Thr 185	Glu	Ser	Trp	Asp 190	Glu	Asp	Tyr
His	His	Gly 195	Gln	Glu	Ser	Leu	His 200	Tyr	Glu	Gly	Arg	Ala 205	Val	Thr	Ile
Ala 210	Thr	Ser	Asp	Arg	Asp	Gln 215	Ser	Lys	Tyr	Gly	Met 220	Leu	Ala	Arg	Leu
Ala 225	Val	Glu	Ala	Gly	Phe 230	Asp	Trp	Val	Ser	Tyr 235	Val	Ser	Arg	Arg	His 240
Ile	Tyr	Cys	Ser	Val 245	Lys	Ser	Asp	Ser	Ser 250	Ile	Ser	Ser	His	Val 255	His
Gly	Cys	Phe 260	Thr	Pro	Glu	Ser	Thr	Ala 265	Leu	Leu	Glu	Ser	Gly 270	Val	Arg
Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr

	275						280						285					
Ala 290	Asn	Gly	Gln	Ala	Val	Tyr 295	Ser	Glu	Val	Ile	Leu 300	Phe	Met	Asp	Arg			
Asn 305	Leu	Glu	Gln	Met	Gln 310	Asn	Phe	Val	Gln	Leu 315	His	Thr	Asp	Gly	Gly 320			
Ala 325	Val	Leu	Thr	Val	Thr	Pro	Ala	His	Leu 330	Val	Ser	Val	Trp	Gln	Pro			
Glu 340	Ser	Gln	Lys	Leu	Thr	Phe	Val	Phe	Ala 345	His	Arg	Ile	Glu	Glu	Lys			
Asn 355	Gln	Val	Leu	Val	Arg	Asp	Val 360	Glu	Thr	Gly	Glu	Leu 365	Arg	Pro	Gln			
Arg 370	Val	Val	Lys	Leu	Gly	Ser	Val 375	Arg	Ser	Lys	Gly	Val	Val	Ala	Pro			
Leu 385	Thr	Arg	Glu	Gly	Thr 390	Ile	Val	Val	Asn	Ser 395	Val	Ala	Ala	Ser	Cys 400			
Tyr 405	Ala	Val	Ile	Asn	Ser	Gln	Ser	Leu	Ala 410	His	Trp	Gly	Leu	Ala	Pro			
Met 420	Arg	Leu	Leu	Ser	Thr	Leu	Glu	Ala 425	Trp	Leu	Pro	Ala	Lys	Glu	Gln			
Leu 435	His	Ser	Ser	Pro	Lys	Val	Val 440	Ser	Ser	Ala	Gln	Gln	Gln	Asn	Gly			
Ile 450	His	Trp	Tyr	Ala	Asn	Ala 455	Leu	Tyr	Lys	Val	Lys	Asp	Tyr	Val	Leu			
Pro 465	Gln	Ser	Trp	Arg	His 470	Asp												

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys	Gly	Pro	Gly	Arg	Gly	Xaa	Gly	Xaa	Arg	Arg	His	Pro	Lys	Lys	Leu
1				5					10					15	
Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr
			20					25					30		
Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Xaa	Arg	Asn	Ser	Glu
		35					40					45			

Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys
50						55					60				
Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys
65					70					75					80
Asp	Lys	Leu	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	Pro	Gly
			85						90					95	
Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Xaa
			100					105					110		
Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser
		115					120					125			
Asp	Arg	Asp	Xaa	Ser	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	Val	Glu
	130					135					140				
Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys
145					150					155					160
Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe
				165					170					175	
Pro	Gly	Ser	Ala	Xaa	Val	Xaa	Leu	Xaa	Xaa	Gly	Gly	Xaa	Lys	Xaa	Val
			180					185					190		
Lys	Asp	Leu	Xaa	Pro	Gly	Asp	Xaa	Val	Leu	Ala	Ala	Asp	Xaa	Xaa	Gly
		195					200					205			
Xaa	Leu	Xaa	Xaa	Ser	Asp	Phe	Xaa	Xaa	Phe	Xaa	Asp	Arg			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys	Gly	Pro	Gly	Arg	Gly	Xaa	Xaa	Xaa	Arg	Arg	Xaa	Xaa	Xaa	Pro	Lys
1				5					10					15	
Xaa	Leu	Xaa	Pro	Leu	Xaa	Tyr	Lys	Gln	Phe	Xaa	Pro	Xaa	Xaa	Xaa	Glu
			20					25					30		
Xaa	Thr	Leu	Gly	Ala	Ser	Gly	Xaa	Xaa	Glu	Gly	Xaa	Xaa	Xaa	Arg	Xaa
		35					40					45			
Ser	Glu	Arg	Phe	Xaa	Xaa	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile
	50					55					60				

Phe	Lys	Asp	Glu	Glu	Asn	Xaa	Gly	Ala	Asp	Arg	Leu	Met	Thr	Xaa	Arg
65					70					75					80
Cys	Lys	Xaa	Xaa	Xaa	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp
				85					90					95	
Pro	Gly	Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Xaa	Asp	Glu	Asp	Gly	His
			100					105					110		
His	Xaa	Xaa	Xaa	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Xaa	Asp	Ile	Thr
		115					120					125			
Thr	Ser	Asp	Arg	Asp	Xaa	Xaa	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala
	130					135					140				
Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Xaa	Xaa	His	Xaa
145					150					155					160
His	Xaa	Ser	Val	Lys	Xaa	Xaa									
				165											

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